

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> Nucleotide sequences which code for the sigE gene

<130> 000445 BT

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15 <170> Patent In Ver. 2.1

<210> 1

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<212> DNA

20 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (302)..(949)

25 <223> sigE gene

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 gtccggtttca gtagtggact cgacataagt gcgaagatac tcgaaggcgt tactcacgcg 180
 ttatagtcta gagcgcgagcag gcgagatgtg aagtacctac acgcattaag tgcaaatgaa 240
 ttcacaattg ccagaagatg cacaggatgt aatctagatt tccaagtgc agtggggcaa 300
 a atg act tat atg aaa aag aag tcc cga gat gac gca ccc gtc gta atc 349
 Met Thr Tyr Met Lys Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile
 1 5 10 15

40 gaa acc gtt caa gca gaa cat gct gaa gaa ctc acg ggc act gca gca 397
 Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala
 20 25 30

45 ttc gat gct gga cag gca gac atg cca aca tgg ggc gag cta gtc gca 445
 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala
 35 40 45

50 gaa cat gca gat agc gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac 493
 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn
 50 55 60

55 cag cac gat gct gaa gac ctg acc caa gaa aca ttc atg cgt gtc ttc 541
 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
 65 70 75 80

cgc tcg ttg aag agc tac cag cca ggc acc ttt gag ggc tgg ctg cac 589
 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
 85 90 95

Sub A1

5 cgc atc acc acc aac ttg ttc ctt gat atg gtt cgc cac cgc ggc aag 637
 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
 100 105 110
 atc cgc atg gag gcg ctg cct gaa gat tat gag cgc gtt ccg ggc aat 685
 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
 115 120 125
 10 gac atc acc cca gag cag gca tac acc gaa gct aac ctt gac cca gct 733
 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
 130 135 140
 15 ctg cag gca gcc ctc gat gag ttg agc cca gac ttc cgc gtg gca gtg 781
 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val
 145 150 155 160
 20 atc ctc tgt gat gtt gtt ggt atg agc tat gac gaa atc gca gag acc 829
 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
 165 170 175
 ctc gga gtg aaa atg ggt acc gtg cgt tcc cgt att cac cgt gga cgc 877
 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg
 180 185 190
 25 agc cag ctt cgt gca agt ttg gaa gct gca gca atg acc agc gag gaa 925
 Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu
 195 200 205
 30 gtt tct ttg ttg gtt cca acc cac taaagttggt gtgttttctg acacgacaaa 979
 Val Ser Leu Leu Val Pro Thr His
 210 215
 35 cgcaaagtgc gtgtcatttt tgcagctcag tgcattattt tggggttcgt ggtgcggaca 1039
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 50 <213> Corynebacterium glutamicum
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 20 25 30

Sub A1

5 Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala
35 40 45

10 Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn
50 55 60

15 Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
65 70 75 80

20 Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
85 90 95

25 Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
100 105 110

30 Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
115 120 125

35 Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
130 135 140

40 Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val
145 150 155 160

45 Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
165 170 175

50 Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg
180 185 190

55 Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu
195 200 205

60 Val Ser Leu Leu Val Pro Thr His
210 215

40 <210> 3
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<212> DNA
<213> Corynebacterium glutamicum

45 <220>
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aacgaatata ttcatacgcg tcacgtgctg cttgggtgac acgatacctg cgggtttgat 120
ccgcaatggt gccgtcaagg agcgcacatcg cgagcaccag cgcaccgcct cgtcgaagaa 180
gcggccaggc ggcgtcgaca agcgccttta aatccatggg ggagacttgg ccgaagacaa 240
gctgatagct gtcgttggca aggcgactca tcacgtcgag cgggcgcgag agcaagaagc 300
gtacgcggct gggggaatag ccggcctcgc ggaagagtgc tttggcctgg cgtgatgct 360
ctgattcagg atcaatgcag gtcagtgtgg tggtatcggc cagtccgttc aggatataca 420
55 gaccaccaa cccggcagcc ggggtaatcg cgatggc 457

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<212> DNA

<213> Corynebacterium glutamicum

<220>

5 <223> downstream region

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 tccgctcaga gtgcaaaaac gaagaagtgt ccgcccgaat ggacctcaaa gcacggcttg 180
 ccagcctcgc cactgagtgc atgcctggcc ctggcgcgaga gaatttagca atgcagcgcc 240
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15 <210> 5

<211> 2086

<212> DNA

<213> Corynebacterium glutamicum

20 <220>

<221> CDS

<222> (759)..(1406)

<223> sigE

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 30 ccgcaatggt gccgtcaagg agcgcatcgg cgagcaccag cgcaccgcct cgtcgaagaa 180
 gcggccaggc ggcgtcgaca agcgcttcta aatccatggg ggagacttgg ccgaagacaa 240
 gctgatagct gtcgttgga aggcgactca tcacgtcgag cgggcgcgag agcaagaagc 300
 35 gtacgcggct gggggaatag ccggcctcgc ggaagagtgc tttggcctgg cgctgatgct 360
 ctgattcagg atcaatgcag gtcagtgtgg tgttatcggc cagtccgttc aggatataca 420
 40 gaccaccaa cccggcagcc ggggtaatcg cgatggcacc agtggagccg ttgccattgg 480
 tgggtggcagc caaagtgggt agcagctggc cagtcatttc atccggggcg gggagaccga 540
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 45 cataagtgcg aagatactcg aaggcgttac tcacgcgtta tagtctagag cgagcaggcg 660
 agatgtgaag tacctacag cattaagtgc aaatgaattc acaattgcca gaagatgcac 720
 50 aggatgtaat ctagatttcc caagttcagt ggggcaaa atg act tat atg aaa aag 776
 Met Thr Tyr Met Lys Lys
 1 5
 aag tcc cga gat gac gca ccc gtc gta atc gaa acc gtt caa gca gaa 824
 55 Lys Ser Arg Asp Asp Ala Pro Val Ile Glu Thr Val Gln Ala Glu
 10 15 20

Sub A1

	cat gct gaa gaa ctc acg ggc act gca gca ttc gat gct gga cag gca	872
	His Ala Glu Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln Ala	
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5	gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc gtt	920
	Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser Val	
	40 45 50	
10	tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa gac	968
	Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn Gln His Asp Ala Glu Asp	
	55 60 65 70	
15	ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc tac	1016
	Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser Tyr	
	75 80 85	
20	cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac ttg	1064
	Gln Pro Gly Thr Phe Glu Gly Trp Leu His Arg Ile Thr Thr Asn Leu	
	90 95 100	
25	ttc ctt gat atg gtt cgc cac cgc ggc aag atc cgc atg gag gcg ctg	1112
	Phe Leu Asp Met Val Arg His Arg Gly Lys Ile Arg Met Glu Ala Leu	
	105 110 115	
30	cct gaa gat tat gag cgc gtt ccg ggc aat gac atc acc cca gag cag	1160
	Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn Asp Ile Thr Pro Glu Gln	
	120 125 130	
35	gca tac acc gaa gct aac ctt gac cca gct ctg cag gca gcc ctc gat	1208
	Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala Leu Gln Ala Ala Leu Asp	
	135 140 145 150	
40	gag ttg agc cca gac ttc cgc gtg gca gtg atc ctc tgt gat gtt gtt	1256
	Glu Leu Ser Pro Asp Phe Arg Val Ala Val Ile Leu Cys Asp Val Val	
	155 160 165	
45	ggt atg agc tat gac gaa atc gca gag acc ctc gga gtg aaa atg ggt	1304
	Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met Gly	
	170 175 180	
50	acc gtg cgt tcc cgt att cac cgt gga cgc agc cag ctt cgt gca agt	1352
	Thr Val Arg Ser Arg Ile His Arg Gly Arg Ser Gln Leu Arg Ala Ser	
	185 190 195	
55	ttg gaa gct gca gca atg acc agc gag gaa gtt tct ttg ttg gtt cca	1400
	Leu Glu Ala Ala Ala Met Thr Ser Glu Glu Val Ser Leu Leu Val Pro	
	200 205 210	
60	acc cac taaagttggt gtgttttctg acacgacaaa cgaaaatgtc gtgtcatttt	1456
	Thr His	
	215	
65	tgcagctcag tgcattattt tggggttcgt ggtgcggaca ggaacttat cacaggcgac	1516
70	atccgttttg agtagtaggt atcttgata agaagttacc cacatccttg aaagtcgaga	1576
75	cacaggaggt catcggaaga tatgttcaat tccgacacca ccgcaatct ccaagctaaa	1636
80	agtcgagatc gtgcaggatc taaagcaaag cgcagcaggc caagttttga ttcagtagcg	1696

Sub A1

5

cgggatgttt tggatgttcg aacaaaaaca gcacaagtta aaaacaaggc taaagagttt 1756

tcctctgttg atcacctttc agcagacgcc gcagccatgt ttgtagacaa tgaactgtcc 1816

cgtggcgcca tgcacgcgc caggctgcac attgtgcact gcgctgaatg tagggaagag 1876

attaaccgtc agcgggaaac cgttgattat ctccgctcag agtgcaaaaa cgaagaagtg 1936

10

tccgccccaa tggacctcaa agcacggctt gccagcctcg cactgagtg catgcctggc 1996

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<213> Corynebacterium glutamicum

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20 25 30

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Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala
35 40 45Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn
50 55 60

35

Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe
65 70 75 80

40

Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His
85 90 95Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys
100 105 110

45

Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn
115 120 125Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala
130 135 140

50

Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val
145 150 155 160Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr
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Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg
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Sub A1

Val Ser Leu Leu Val Pro Thr His
210 215

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<220>
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